FIG. 1A

```
aagcggccggtctgcagtcggagacttgcaggcagcaaacacggtgcgaacgaaccggagggggggagagagaaatcaaacagctaagcgt   90
ggagcagacggcctgggacccagaagggggatcgatgcgaggagcgcaataataacaacaataataacccacttcggagcaaacagcatat  180
aaagagctgcgacccaactgcagcctaaaaaaaatcaaacctgctcatgcacc                                       232
```

```
              10                  20                  30
    M V V Q T R F P S W I I L C Y I W L L G F A H T G E A Q A A
    ATGGTTGTTCAAACTCGGTTCCCTTCGTGGATTATTTTTGTGTTACATCTGGCTGCTTGGCTTTGCACACACGGGGGAGGCGCAGGCTGCG   322

              40                  50                  60
    K E V L L L L D S K A Q Q T E L E W I S S P P S G W E E I S G
    AAGGAAGTACTATTACTGGACTCGAAAGCACAACAAACAGAATTGGAATGGATTTCCTCTCCACCCAGTGGGTGGGAAGAAATTAGTGGT   412

              70                  80                  90
    L D E N Y T P I R T Y Q V C Q V M E P N Q N N W L R T N W :
    TTGGATGAGAACTACACTCCGATAAGAACATACCAGGTGTGCCAGGTCATGGAGCCCAACCAGAACAACTGGCTGCGGACTAACTGGATT   502

             100                 110                 120
    S K G N A Q R I F V E L K F T L R D C N S L P G V L G T C K
    TCTAAAGGCAACGCACAAAGGATTTTTGTAGAATTGAAATTCACCTTGAGGGATTGTAATAGTCTTCCCGGAGTCCTGGGAACTTGCAAG   592

             130                 140                 150
    E T F N L Y Y Y E T D Y D T G R N I R E N L Y V K I D T I A
    GAAACGTTTAATTTGTACTATTATGAAACAGACTACGACACCGGCAGGAATATACGAGAAAACCTTTATGTTAAAATAGACACCATTGCT   682

             160                 170                 180
    A D E S F T Q G D L G E R K M K L N T E V R E I G P L S K E
    GCAGATGAAAGTTTCACACAAGGTGACCTTGGTGAAAGAAAGATGAAGCTGAACACTGAGGTGAGAGAGATTGGACCTTTGTCCAAAAAG   772

             190                 200                 210
    G F Y L A F Q D V G A C I A L V S V K V Y Y K K C W T I V E
    GGATTCTATCTTGCCTTTCAGGATGTAGGGGCTTGCATAGCATTGGTTTCTGTCAAAGTGTACTACAAGAAGTGCTGGACCATTGTTGAG   862

             220                 230                 240
    N L A V F P D T V T G S E F S S L V E V R G T C V S S A E E
    AACTTAGCTGTCTTTCCAGATACAGTGACTGGTTCGGAATTTTCCTCCTTAGTCGAGGTCCGTGGGACATGTGTCAGCAGTGCCGAGGAA   952

             250                 260                 270
    E A E N S P R M H C S A E G E W L V P I G K C I C K A G Y Q
    GAGGCAGAAAATTCCCCCAGAATGCATTGCAGTGCAGAAGGAGAGTGGCTAGTACCCATTGGAAAATGCATCTGCAAAGCAGGCTATCAG   1042

             280                 290                 300
    Q K G D T C E P C G R R F Y K S S S Q D L Q C S R C P T H S
    CAAAAAGGGGACACTTGCGAACCCTGTGGCCGCAGGTTCTACAAATCTTCCTCTCAGGATCTCCAGTGTTCTCGTTGTCCAACCCACAGC   1132

             310                 320                 330
    F S D R E G S S R C E C E D G Y Y R A P S D P P Y V A C T R
    TTCTCTGACCGAGAAGGATCATCCAGGTGTGAATGTGAAGATGGGTACTACAGAGCTCCTTCTGATCCACCATACGTTGCATGCACGAGG   1222

             340                 350                 360
    P P S A P Q N L I F N I N Q T T V S L E W S P P A D N G G R
    CCTCCCTCTGCACCACAGAACCTTATTTTTCAATATCAATCAAACGACTGTAAGTTGGAATGGAGTCCTCCGGCTGACAACGGGGGAAGA   1312

             370                 380                 390
    N D V T Y R I L C K R C S W E Q G E C V P C G S N I G Y M P
    AACGATGTCACCTACAGAATACTGTGTAAGCGGTGCAGTTGGGAACAGGGAGAATGTGTGCCATGCGGAAGTAACATTGGATACATGCCC   1402

             400                 410                 420
    Q Q T G L E D N Y V T V M D L L A E A N Y T F E V E A V N G
    CAGCAGACGGGATTAGAGGATAACTATGTCACTGTCATGGACCTACTTGCCCATGCAAATTACACTTTCGAAGTTGAAGCTGTAAATGGA   1492

             430                 440                 450
    V S D L S R S Q R L F A A V S I T T G Q A A P S Q V S G V M
    GTTTCGGACTTAAGCAGATCCCAGAGGCTCTTCGCTGCTGTTAGCATCACCACCGGTCAAGCAGCTCCCTCGCAAGTGAGTGGAGTCATG   1582

             460                 470                 480
    K E R V L Q R S V Q L S W Q E P E E P N G V I T E Y E I K Y
    AAGGAGCGAGTACTGCAGCGGAGTGTGCAGCTTTCCTGGCAGGAGCCGGAGCATCCCAATGGAGTCATCACGGAATATGAAATCAAGTAT   1672

             490                 500                 510
    Y E K D Q R E R T Y S T L K T K S T S A S I N N L K P G T V
    TATGAGAAAGATCAACGGGAAAGGACGTACTCAACACTCAAAACCAAGTCCACCTCCGCCTCCATTAATAATCTGAAACCGGGAACAGTG   1762

             520                 530                 540
    Y V F Q I R A V T A A G T G N Y S P R L D V A T L E E A S G
    TACGTCTTTCAGATCCGGGCGGTCACTGCTGCCGGTTATGGAAACTACAGCCCTAGGCTTGATGTTGCCACACTTGAGGAAGCTTCAGGT   1852
```

FIG. 1B

```
                    550                        560                        570
K  M  F  E  A  T  A  V  S  S  E  Q  N  P  V  I  I  I  A  V  V  A  V  A  G  T  I  I  L  V
AAAATGTTTGAAGCGACAGCAGTCTCCAGTGAACAGAATCCTGTCATCATAATTGCTGTAGTGGCTGTAGCAGGGACCATCATCTTGGTG  1942

                    580                        590                        600
F  M  V  F  G  F  I  I  G  R  R  H  C  G  Y  S  K  A  D  Q  E  G  D  E  E  L  Y  F  H  F
TTCATGGTGTTCGGCTTCATCATTGGAAGAAGGCACTGTGGTTATAGCAAGGCTGACCAAGAAGGGGATGAAGAACTCTACTTTCATTTT  2032

                    610                        620                        630
K  F  P  G  T  K  T  Y  I  D  P  E  T  Y  E  D  P  N  R  A  V  H  Q  F  A  K  E  L  D  A
AAATTTCCAGGCACCAAAACCTACATTGACCCTGAAACCTATGAGGACCCAAATAGAGCTGTCCATCAATTCGCCAAGGAGCTAGATGCC  2122

                    640                        650                        660
S  C  I  K  I  E  R  V  I  G  A  G  E  F  G  E  V  C  S  G  R  L  K  L  P  G  Q  R  D  V
TCCTGTATTAAAATTGAGCGTGTGATTGGTGCAGGAGAATTTGGAGAAGTTTGCAGTGGTCGTTTGAAACTTCCGGGCCAGAGAGATGTT  2212

                    670                        680                        690
A  V  A  I  K  T  L  K  V  G  Y  T  E  K  Q  R  R  D  F  L  C  E  A  S  I  M  G  Q  F  D
GCAGTGGCCATAAAAACCCTGAAAGTTGGTTACACAGAAAAGCAAAGGAGGGACTTTTTATGCGAAGCAAGCATCATGGGGCAATTTGAC  2302

                    700                        710                        720
H  P  N  V  V  H  L  E  G  V  V  T  R  G  K  P  V  M  I  V  I  E  F  M  E  N  G  A  L  D
CACCCAAATGTCGTCCATTTGGAAGGGGTTGTTACAAGAGGGAAGCCTGTCATGATTGTGATAGAGTTCATGGAGAATGGAGCCCTGGAT  2392

                    730                        740                        750
A  F  L  R  K  H  D  G  Q  F  T  V  I  Q  L  V  G  M  L  R  G  I  A  A  G  M  R  Y  L  A
GCATTTCTCAGGAAACACGATGGGCAGTTTACAGTCATTCAGTTGGTAGGAATGTTGAGAGGTATTGCCGCTGCCATGCGATACTTGGCT  2482

                    760                        770                        780
D  M  G  Y  V  H  R  D  L  A  A  R  N  I  L  V  N  S  N  L  V  C  K  V  S  D  F  G  L  S
GATATGGGATACGTTCACAGGGACCTTGCAGCGCGCAACATCCTTGTCAACAGCAATCTTGTTTGTAAAGTGTCAGATTTTGGCCTTTCC  2572

                    790                        800                        810
R  V  I  E  D  D  P  E  A  V  Y  T  T  T  G  G  K  I  P  V  R  W  T  A  P  E  A  I  Q  Y
CGGGTTATAGAGGATGATCCCGAAGCTGTCTACACCACGACTGGTGGAAAAATTCCAGTAAGGTGGACTGCACCGGAAGCCATTCAATAC  2662

                    820                        830                        840
R  K  F  T  S  A  S  D  V  W  S  Y  G  I  V  M  W  E  V  M  S  Y  G  E  R  P  Y  W  D  M
CGGAAGTTCACCTCAGCCAGCGATGTGTGGAGCTATGGGATTGTCATGTGGGAAGTGATGTCTTATGGAGAAAGACCTTACTGGGACATG  2752

                    850                        860                        870
S  N  Q  D  V  I  K  A  I  E  E  G  Y  R  L  P  A  P  M  D  C  P  A  G  L  H  Q  L  M  L
TCAAATCAAGATGTCATTAAAGCGATAGAAGAAGGTTATCGTTTGCCGGCGCCCATGGATTGCCCAGCTGGTCTTCACCAGCTAATGCTG  2842

                    880                        890                        900
D  C  W  Q  K  D  R  A  E  R  P  K  P  E  Q  I  V  G  I  L  D  K  M  I  R  N  R  S  S  L
GATTGTTGGCAGAAAGATCGGGCGGAAAGGCCAAAGTTTGAGCAGATAGTCGGAATTCTAGACAAAATGATTCGAAACCCAAGTAGTCTG  2932

                    910                        920                        930
K  T  P  L  G  T  C  S  R  P  L  S  P  L  L  D  Q  S  T  P  D  F  T  A  F  C  S  V  G  E
AAAACACCCCTGGGAACTTGTAGTAGACCCCTTAAGCCCTCTTCTGGACCAGAGCACTCCTGACTTCACTGCCTTCTGTTCAGTTGGAGAA  3022

                    940                        950                        960
W  L  Q  A  I  K  M  E  R  Y  K  D  N  F  T  A  A  G  Y  N  S  L  E  S  V  A  R  M  T  I
TGGTTGCAAGCTATTAAAATGGAAAGGTATAAGGACAACTTCACAGCAGCGGGTTACAACTCACTCGAGTCAGTGGCCAGGATGACTATC  3112

                    970                        980                        990
D  D  V  M  S  L  G  I  T  L  V  G  E  Q  K  K  I  M  S  S  I  Q  T  M  R  A  Q  M  L  H
GATGATGTGATGAGTTTAGGGATCACACTGGTTGGCCATCAAAAGAAGATCATGAGCAGCATCCAGACTATGCGGGCACAAATGTTGCAT  3202

L  H  G  T  G  I  Q  V  *
TTACACGGAACAGGCATCCAAGTGTGA                                                              3229
```

```
cacatcggcctccctcagatgaggcttaagactgcaggagaacagttctggccttcagtatacgcatagaatgctgctagaagacagttg  3319
atatactgggtccttcctacaagaaagagaagatttttagaagcacctccagacttgaactcctaagtgccaccagaatatacaaaaaggg  3409
aatttaggatccaccactggtggccaggaacacagcagagacaataaacaaagtactacctgaaaaacatcccaacaccttgagctctcg  3499
aacctcctttttatcttatagactttttaaaaatgtacataaagaaatttaagaaagaatatatttgtcaaataaaaatcatgatcttatt  3589
gttaaaatcaatgaaatattttccttaaaaaaaaaaaa                                                  3628

gttaaaatcaatgaaatattttccttaaaaatatgtgatttcagactattcttttccagaaccatctgtgtttattctgcttaaggacttt  3679
gttttagaaagttatttgtagctttggacctttttagtgttaaatttatgacacgttactacactgggaacctttgaagactctcaaact  3769
taaaggaaagcaaaactacgcacatagtcgaggatggactttgtccttcatggctttggtatcctggctgtgtcattttgttaaaccagt  3859
gatgttttcatattgtttgctgattggcaggtagttcaaaattgcaagttgccaagagctctgatattttttaacaggattttttttttct  3949
ttgtaaaaatcagataacatactaactttttcaatgaaaaaaaaaaaaaaaagaagcaataatgatccataaatactataaggcactttta  4039
cagattgtttatagagtgatttactaggcagaattttaataaaaaaaaaagagagatgtcaaatttttaggtttatgtgtatatgataaaag  4129
gctgagcttcgtctgaagatgctggtgaaagcaagactggaagcgaagctctccagctttggctaacccaatccgagcacatcaagagct  4219
tcagtcttgtgacagtaagaaaatttaggaacatagttgacctatatttttgtattctttcttgttgaatgcagtccaaatacaaaa  4304
```

FIG. 2A

MDK1'-T1

```
              570           580           590
    V  A  V  A  G  T  I  I  L  V  F  M  V  F  G  F  I  I  G  R  R  H  C  G  Y  S  K  A  D  Q
GTGGCTGTGTAGCAGGGACCATCATCATCTTGGTGTTGTTCATGGTGTTCGGCTTCATCATTGGAAGAAGGCACTGTGGTTATAGCAAGGCTGACCAA   2002

                  600                          610
    E  G  D  E  E  L  Y  F  H  S  L  V  T  N  E  H  L  S  V  L  *
GAAGGGGATGAAGAACTCTACTTCATTCTTTAGTAACAAATGAGCACCTGTCAGTTTATAAAaccgcaacaataactgtttaagacaat   2092

caattttggataaacaatcaactacagcagaataaatcaagatttttaagtccattttccttttatacattctgcttatttgttgttat   2182
atgtttatttttaaacctctgatcttgatgaatgtgatacctaagcacagttaggctgcagtgtaaatataataaagacattgttctga   2272
gagcagtacgatttcatggaaagattgttggtggcttgtctttgttaaaattaataaagaatttaaggatatagtgtaattttcttcattgc   2362
attaatataaccaaatatgcctacctatctttgtcttgaaccaaatgaatagattggaatacttttattgaattgataataaag           2452
ttgactgagcatttatgtgttacctgctgatgcttctgggtgtcattgcattgaaatatttaacttttaaaatgatacatgttgttcaattttga   2542
ctacctttgtgaggcatactggctacctcctcctattagctaagatcttccaaagcctataatgaaaagtttatataaaccatttctc      2632
tttcaaatcactgtcatacttggtcacggatcccaggaatattgtaaattttctaattttcatcctgcactttgtatatccagcctctatta      2722
ccctcaaggtgaatataaaactatgtctttgaatatttctctttgattttgtgatagcagtccctcatatcttgtactaatttatgta      2812
tatgtcaacagtggtggttggtctttaaaaataaaatcaaagaatagtaagtaaaaaaataaaaaaaaaaaaaaaa      2901
```
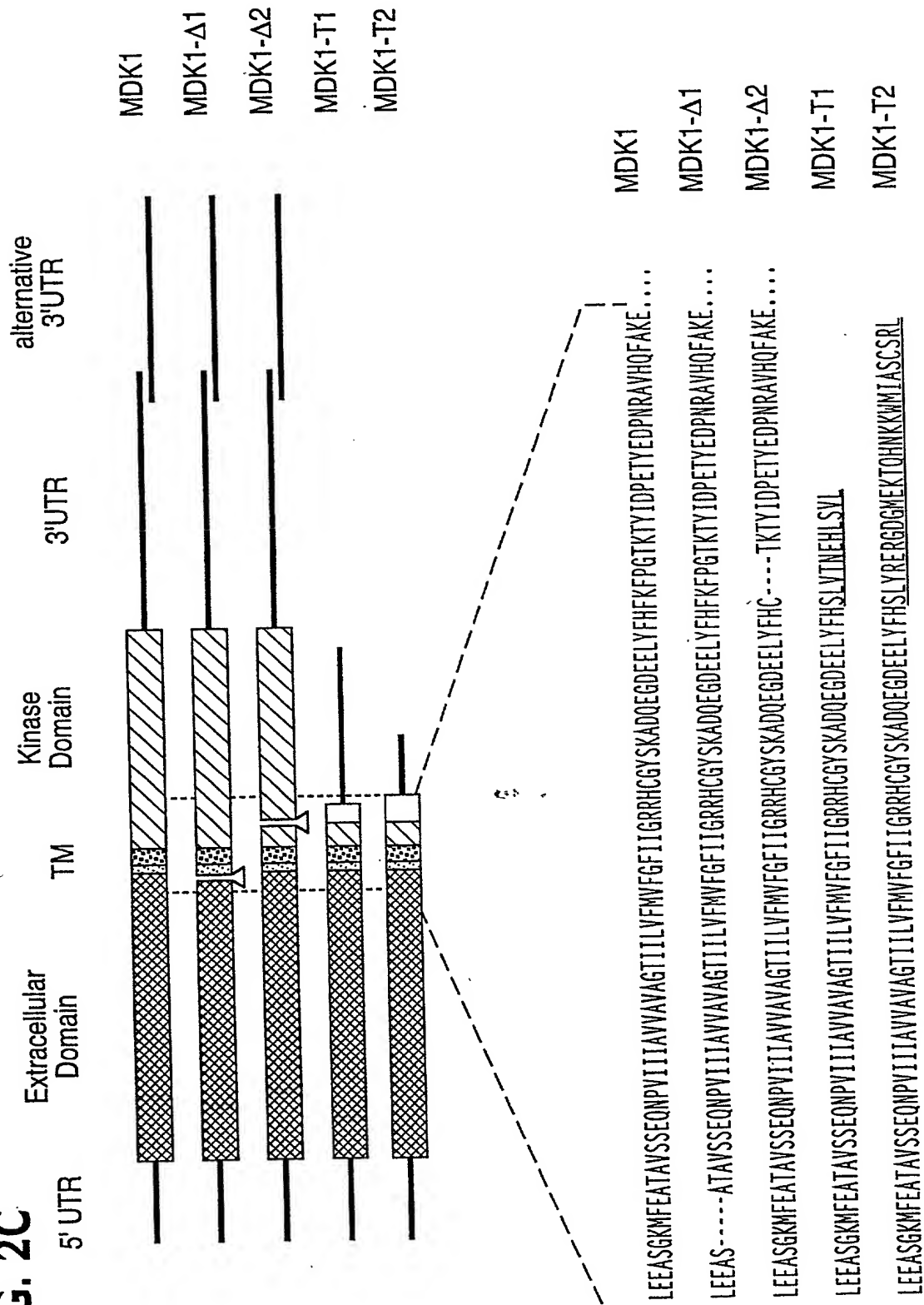
FIG. 2B

MDK1-T2

```
                    570                          580                           590
V  A  V  A  G  T  I  I  L  V  F  M  V  F  G  F  I  I  G  R  R  H  C  G  Y  S  K  A  D  Q
GTGGCTGTGTAGCAGGGACCATCATCTTGGTGTTCATGGTGTTCGGCTTCATCATTGGAAGAAGGCACTGTGGTTATAGCAAGGCTGACCAA  2002
                      600                          610                           620
E  G  D  E  E  L  Y  F  H  S  E  Y  R  E  R  G  D  G  M  E  K  T  Q  H  N  K  K  W  M  I
GAAGGGGATGAAGAACTCTACTTTCATTCTGTTTACAGGGAAGGGGGAGACGGGATGGAAAAGACACAGCACAATAAGAAGTGGATGATT  2092

A  S  C  S  R  L  *
GCATCGTGCTCTCGTTTGTTTAGgtctcttttcctaatcaacactatgatttgaagtacgcgtacacgaagcaaacgggaagagataagga  2182

attagcattgtgaacctgactgtaatcctctctcttccggaaagagatgagatgctattgcgatgagaatgtacaacttgcaccttgaaatc  2272
tttttgataattagtgctcagggggaggggggggaagtagagaaagcaaa  2323
```

FIG. 2C

5' UTR Extracellular Domain TM Kinase Domain 3'UTR alternative 3'UTR

MDK1
MDK1-Δ1
MDK1-Δ2
MDK1-T1
MDK1-T2

MDK1
MDK1-Δ1
MDK1-Δ2
MDK1-T1
MDK1-T2

LEEASGKMFEATAVSSEQNPVIIIAVVAVAGTIILVFMVFGFIIGRRHCGYSKADQEGDEELYFHFKFPGTKTYIDPETYEDPNRAVHQFAKE....

LEEAS----ATAVSSEQNPVIIIAVVAVAGTIILVFMVFGFIIGRRHCGYSKADQEGDEELYFHFKFPGTKTYIDPETYEDPNRAVHQFAKE....

LEEASGKMFEATAVSSEQNPVIIIAVVAVAGTIILVFMVFGFIIGRRHCGYSKADQEGDEELYFHĊ----TKTYIDPETYEDPNRAVHQFAKE....

LEEASGKMFEATAVSSEQNPVIIIAVVAVAGTIILVFMVFGFIIGRRHCGYSKADQEGDEELYFHSLVTNEHLSYL

LEEASGKMFEATAVSSEQNPVIIIAVVAVAGTIILVFMVFGFIIGRRHCGYSKADQEGDEELYFHSLYRERGDGMEKTQHNKKWMIASCSRL

FIG. 3